

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 29, 2004, 14:05:17 ; Search time 193 Seconds
(without alignments)
80.493 Million cell updates/sec

Title: US-10-753-339-25

Sequence: 1 KQIINWQEVGKAMYAKAFSPVPMF 27

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot 02: *
1: uniprot_sprot: *
2: uniprot_trembl: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|--------|--------------------|
| 1 | 94 | 66.2 | 202 | P88521 | P88521 human immun |
| 2 | 94 | 66.2 | 397 | O11557 | O11557 human immun |
| 3 | 94 | 66.2 | 412 | O11561 | O11561 human immun |
| 4 | 93 | 65.5 | 197 | O74009 | O74009 human immun |
| 5 | 93 | 65.5 | 199 | O74005 | O74005 human immun |
| 6 | 93 | 65.5 | 200 | P88475 | P88475 human immun |
| 7 | 93 | 65.5 | 200 | P88514 | P88514 human immun |
| 8 | 93 | 65.5 | 200 | P88516 | P88516 human immun |
| 9 | 93 | 65.5 | 200 | P88519 | P88519 human immun |
| 10 | 93 | 65.5 | 200 | O73980 | O73980 human immun |
| 11 | 93 | 65.5 | 200 | O73981 | O73981 human immun |
| 12 | 93 | 65.5 | 200 | O74003 | O74003 human immun |
| 13 | 93 | 65.5 | 200 | O74004 | O74004 human immun |
| 14 | 93 | 65.5 | 200 | O9QE80 | O9QE80 human immun |
| 15 | 93 | 65.5 | 200 | O9QE81 | O9QE81 human immun |
| 16 | 93 | 65.5 | 200 | O9QE82 | O9QE82 human immun |
| 17 | 93 | 65.5 | 201 | O73995 | O73995 human immun |
| 18 | 93 | 65.5 | 201 | O74010 | O74010 human immun |
| 19 | 93 | 65.5 | 201 | O9QE83 | O9QE83 human immun |
| 20 | 93 | 65.5 | 201 | O9QE84 | O9QE84 human immun |
| 21 | 93 | 65.5 | 202 | P88444 | P88444 human immun |
| 22 | 93 | 65.5 | 202 | P88445 | P88445 human immun |
| 23 | 93 | 65.5 | 202 | P88446 | P88446 human immun |
| 24 | 93 | 65.5 | 202 | P88447 | P88447 human immun |
| 25 | 93 | 65.5 | 202 | P88448 | P88448 human immun |
| 26 | 93 | 65.5 | 202 | P88449 | P88449 human immun |
| 27 | 93 | 65.5 | 202 | P88450 | P88450 human immun |
| 28 | 93 | 65.5 | 202 | P88451 | P88451 human immun |
| 29 | 93 | 65.5 | 202 | P88452 | P88452 human immun |
| 30 | 93 | 65.5 | 202 | P88453 | P88453 human immun |
| 31 | 93 | 65.5 | 202 | P88489 | P88489 human immun |

| | | | | | | |
|----|----|------|-----|---|--------|--------------------|
| 32 | 93 | 65.5 | 202 | 2 | P88490 | P88490 human immun |
| 33 | 93 | 65.5 | 202 | 2 | P88495 | P88495 human immun |
| 34 | 93 | 65.5 | 202 | 2 | P88498 | P88498 human immun |
| 35 | 93 | 65.5 | 202 | 2 | P88499 | P88499 human immun |
| 36 | 93 | 65.5 | 202 | 2 | P88500 | P88500 human immun |
| 37 | 93 | 65.5 | 202 | 2 | P88501 | P88501 human immun |
| 38 | 93 | 65.5 | 202 | 2 | P88502 | P88502 human immun |
| 39 | 93 | 65.5 | 202 | 2 | P88503 | P88503 human immun |
| 40 | 93 | 65.5 | 202 | 2 | P88504 | P88504 human immun |
| 41 | 93 | 65.5 | 202 | 2 | P88505 | P88505 human immun |
| 42 | 93 | 65.5 | 202 | 2 | P88506 | P88506 human immun |
| 43 | 93 | 65.5 | 202 | 2 | P88509 | P88509 human immun |
| 44 | 93 | 65.5 | 202 | 2 | P88510 | P88510 human immun |
| 45 | 93 | 65.5 | 202 | 2 | P88512 | P88512 human immun |

ALIGNMENTS

RESULT 1
P88521 PRELIMINARY; PRT; 202 AA.
AC P88521; (Tremblrel. 03, Created)
DT 01-MAY-1997 (Tremblrel. 03, Last sequence update)
DT 01-MAY-1997 (Tremblrel. 03, Last sequence update)
DE 01-JUN-2003 (Tremblrel. 24, Last annotation update)
DE Envelope glycoprotein, V3-V5 region (Fragment).
GN Name-env;
OS Human immunodeficiency virus 1.
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OC NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97296232; PubMed=9151816;
RA Liu S.L., Schacker T., Musey L., Shriner D., McElrath M.J., Corey L., Mullins J.I.;
RT "Divergent patterns of progression to AIDS after infection from the same source: human immunodeficiency virus type 1 evolution and antiviral responses.";
RT J. Virol. 71:4284-4295(1997).
RL [2]
RP SEQUENCE FROM N.A.
RA Liu S.-L., Shacker T., Musey L., McElrath M.J., Corey L., Mullins J.I.;
RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U79112; AAC57411.1; -;
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
KW AIDS; Coat protein; Envelope protein; Glycoprotein; Transmembrane.
FT NON_TER 1
FT NON_TER 202
SQ SEQUENCE 202 AA; 22411 MW; A6257A189FE04103 CRC64;
Query Match 66.2%; Score 94; DB 2; Length 202;
Best Local Similarity 82.6%; Pred. No. 4.6e-06;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 KQIINWQEVGKAMYAKAFSPV 23
Db 146 KQIINWQEVGKAMYAPPISGEV 168

RESULT 2
O11557 PRELIMINARY; PRT; 397 AA.
ID O11557
AC O11557; (Tremblrel. 04, Created)
DT 01-JUL-1997 (Tremblrel. 04, Last sequence update)
DT 01-JUL-1997 (Tremblrel. 04, Last sequence update)
DE 01-JUN-2003 (Tremblrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).

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OM protein - protein search, using sw model

Run on: December 29, 2004, 14:29:56 ; Search time 38 Seconds
(without alignments)
68.365 Million cell updates/sec

Title: US-10-753-339-25

Perfect score: 142
Sequence: 1 KOIINWQEVGKAMKAFSPVPMF 27

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:*

1: piri: *
2: pir2: *
3: pir3: *
4: pir4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|-----------|---------------------|
| 1 | 90 | 63.4 | 851 | 2 S33985 | env polyprotein - |
| 2 | 90 | 63.4 | 856 | 1 VCLJH3 | env polyprotein pr |
| 3 | 86 | 60.6 | 506 | 2 A40218 | envelop glycoprote |
| 4 | 86 | 60.6 | 854 | 2 S13288 | env protein - huma |
| 5 | 86 | 60.6 | 855 | 1 VCLJAJ2 | env polyprotein pr |
| 6 | 86 | 60.6 | 856 | 1 VCLJVL | env polyprotein pr |
| 7 | 86 | 60.6 | 859 | 1 VCLJMN | env polyprotein pr |
| 8 | 86 | 60.6 | 861 | 1 VCLJLV | env polyprotein pr |
| 9 | 85 | 59.9 | 290 | 2 S25940 | env protein - huma |
| 10 | 85 | 59.9 | 297 | 2 S60538 | envelope polyprote |
| 11 | 85 | 59.9 | 443 | 2 C41621 | env polyprotein P |
| 12 | 85 | 59.9 | 843 | 1 H44001 | env polyprotein pr |
| 13 | 85 | 59.9 | 847 | 2 T09448 | env polyprotein pr |
| 14 | 85 | 59.9 | 852 | 1 VCLJBR | envelope glycoprot |
| 15 | 84 | 59.2 | 445 | 2 A41621 | env polyprotein - |
| 16 | 84 | 59.2 | 454 | 2 B41621 | env polyprotein M |
| 17 | 84 | 59.2 | 729 | 1 VCLJJK | env polyprotein pr |
| 18 | 84 | 59.2 | 861 | 1 VCLJSC | env polyprotein pr |
| 19 | 84 | 59.2 | 861 | 1 VCLJKB | env protein - huma |
| 20 | 81 | 57.0 | 847 | 2 S13289 | envelope polyprote |
| 21 | 80.5 | 56.7 | 300 | 2 S60522 | envelope polyprote |
| 22 | 80 | 56.3 | 300 | 2 S60546 | envelope polyprote |
| 23 | 80 | 56.3 | 300 | 2 S60547 | envelope polyprote |
| 24 | 80 | 56.3 | 301 | 2 S60548 | envelope polyprote |
| 25 | 79 | 55.6 | 294 | 2 S60525 | envelope polyprote |
| 26 | 79 | 55.6 | 852 | 2 T12016 | envelope glycoprot |
| 27 | 79 | 55.6 | 853 | 2 S54384 | envelope glycoprote |
| 28 | 79 | 55.6 | 855 | 1 VCLJZR | env polyprotein pr |
| 29 | 79 | 55.6 | 856 | 1 VCLJ3W | env polyprotein pr |

| | | | | | |
|----|------|------|-----|----------|--------------------|
| 30 | 78 | 54.9 | 495 | 2 S31493 | env polyprotein - |
| 31 | 77.5 | 54.6 | 299 | 2 S60552 | envelope polyprote |
| 32 | 77.5 | 54.6 | 299 | 2 S60551 | envelope polyprote |
| 33 | 77.5 | 54.6 | 299 | 2 S60554 | envelope polyprote |
| 34 | 77.5 | 54.6 | 299 | 2 S60553 | envelope polyprote |
| 35 | 77 | 54.2 | 859 | 2 T01672 | envelope polyprote |
| 36 | 76 | 53.5 | 294 | 2 S60545 | envelope polyprote |
| 37 | 76 | 53.5 | 294 | 2 S60524 | envelope polyprote |
| 38 | 76 | 53.5 | 846 | 1 VCLJND | env polyprotein pr |
| 39 | 75.5 | 53.2 | 303 | 2 S60549 | envelope polyprote |
| 40 | 75.5 | 53.2 | 303 | 2 S60550 | envelope polyprote |
| 41 | 75 | 52.8 | 301 | 2 S60532 | envelope polyprote |
| 42 | 75 | 52.8 | 301 | 2 S60531 | envelope polyprote |
| 43 | 75 | 52.8 | 856 | 1 A4963 | env polyprotein pr |
| 44 | 74.5 | 52.5 | 299 | 2 S60521 | envelope polyprote |
| 45 | 74.5 | 52.5 | 299 | 2 S60523 | envelope polyprote |

ALIGNMENTS

RESULT 1

S33985
env polyprotein - human immunodeficiency virus type 1
C:Species: human immunodeficiency virus type 1, HIV-1
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C:Accession: S33985
R;Carlini, F.
submitted to the EMBL Data Library, November 1991
A:Reference number: S33979
A:Accession: S33985
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-851 <CAR>
C:Cross-references: UNIPROT:O78243; EMBL:Z11530; NID:G60192; PIDN:CAA77628.1; PID:G601
C:Superfamily: type E retrovirus env polyprotein

Query Match 63.4%; Score 90; DB 2; Length 851;
Best Local Similarity 73.9%; Pred. No. 2.1e-05;
Matches 17; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 KOIINWQEVGKAMKAFSPV 23
DB 416 KOIINWQEVGKAMYAPISGQI 438
|||||
|::

RESULT 2

VCLJH3
env polyprotein precursor - human immunodeficiency virus type 1 (isolate HTLV-III, BH1
N:Alternate names: coat polyprotein
C:Species: human immunodeficiency virus type 1, HIV-1
A:Note: host Homo sapiens (man)
C:Date: 17-May-1985 #sequence_revision 17-May-1985 #text_change 09-Jul-2004
C:Accession: A03973
R;Ratner, L.; Haseltine, W.; Patarca, R.; Livak, K.J.; Starcich, B.; Josephs, S.F.; Do
nberger, J.A.; Papas, T.S.; Ghrayeb, J.; Chang, N.T.; Gallo, R.C.; Wong-Staal, F.
Nature 313, 277-284, 1985
A:Title: Complete nucleotide sequence of the AIDS virus, HTLV-III.
A:Reference number: A93353; MUID:85111123; PMID:2578615
A:Accession: A03973
A:Molecule type: DNA
A:Residues: 1-856 <RAT>
A:Cross-references: UNIPROT:P03375; GB:M15654; GB:K02008; GB:K02009; GB:K02010; NID:G3
C:Genetics:
A:Gene: env
C:Superfamily: type E retrovirus env polyprotein
C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polypr
F:1-30/Domain: signal sequence #status predicted <SIG>
F:31-511/Product: exterior membrane glycoprotein #status predicted <EXT>
F:512-856/Product: transmembrane glycoprotein #status predicted <TMMS>
P:88,136,141,156,160,186,197,230,234,241,262,276,289,295,301,332,339,356,386,392,397,4
P:611,616,625,637,674,750,816/Binding site: carbohydrate (Asn) (covalent) #status pred

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OM protein - protein search, using sw model

Run on: December 29, 2004, 14:37:51 ; Search time 465 Seconds
(without alignments)

64.335 Million cell updates/sec

Title: US-10-753-339-25

Perfect score: 142

Sequence: 1 KQIINWQEVGKMYAKAFSEVPMF 27

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 6730630 seqs, 1107998698 residues

Total number of hits satisfying chosen parameters: 6730630

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Pending Patents AA Main.*
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2: /cgn2_6/ptodata/1/paa/US06 COMB.pcp.*
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5: /cgn2_6/ptodata/1/paa/US08 COMB.pcp.*
6: /cgn2_6/ptodata/1/paa/US08 COMB.pcp.*
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35: /cgn2_6/ptodata/1/paa/US10 COMB.pcp.*
36: /cgn2_6/ptodata/1/paa/US10 COMB.pcp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

*

Query Match

100.0%; Score 142; DB 1; Length 27;

| Result No. | Score | Query Match | Length | DB | ID | Description |
|------------|-------|-------------|--------|----|----------------------|--------------------|
| 1 | 142 | 100.0 | 27 | 1 | PCT-US01-03540-25 | Sequence 25, Appl |
| 2 | 142 | 100.0 | 27 | 1 | PCT-US01-03540-102 | Sequence 102, App |
| 3 | 142 | 100.0 | 27 | 1 | PCT-US01-03540A-25 | Sequence 25, Appl |
| 4 | 142 | 100.0 | 27 | 1 | PCT-US01-03540A-102 | Sequence 102, App |
| 5 | 142 | 100.0 | 27 | 22 | US-09-775-805-25 | Sequence 25, Appl |
| 6 | 142 | 100.0 | 27 | 22 | US-09-775-805-102 | Sequence 102, App |
| 7 | 142 | 100.0 | 27 | 22 | US-09-775-805A-25 | Sequence 25, Appl |
| 8 | 142 | 100.0 | 27 | 22 | US-09-775-805A-102 | Sequence 102, App |
| 9 | 142 | 100.0 | 27 | 22 | US-10-753-339-25 | Sequence 25, Appl |
| 10 | 142 | 100.0 | 27 | 22 | US-10-753-339-102 | Sequence 102, App |
| 11 | 94 | 66.2 | 202 | 22 | US-09-791-537-45937 | Sequence 45937, A |
| 12 | 93 | 65.5 | 197 | 22 | US-09-791-537-86890 | Sequence 86890, A |
| 13 | 93 | 65.5 | 200 | 22 | US-09-791-537-45525 | Sequence 45525, A |
| 14 | 93 | 65.5 | 200 | 22 | US-09-791-537-45920 | Sequence 45920, A |
| 15 | 93 | 65.5 | 200 | 22 | US-09-791-537-45923 | Sequence 45923, A |
| 16 | 93 | 65.5 | 200 | 22 | US-09-791-537-45934 | Sequence 45934, A |
| 17 | 93 | 65.5 | 200 | 22 | US-09-791-537-77855 | Sequence 77855, A |
| 18 | 93 | 65.5 | 200 | 22 | US-09-791-537-77857 | Sequence 77857, A |
| 19 | 93 | 65.5 | 200 | 22 | US-09-791-537-77860 | Sequence 77860, A |
| 20 | 93 | 65.5 | 200 | 22 | US-09-791-537-86791 | Sequence 86791, A |
| 21 | 93 | 65.5 | 200 | 22 | US-09-791-537-86792 | Sequence 86792, A |
| 22 | 93 | 65.5 | 201 | 22 | US-09-791-537-77836 | Sequence 77836, A |
| 23 | 93 | 65.5 | 201 | 22 | US-09-791-537-77852 | Sequence 77852, A |
| 24 | 93 | 65.5 | 201 | 22 | US-09-791-537-135944 | Sequence 135944, A |
| 25 | 93 | 65.5 | 202 | 22 | US-09-791-537-45468 | Sequence 45468, A |
| 26 | 93 | 65.5 | 202 | 22 | US-09-791-537-45470 | Sequence 45470, A |
| 27 | 93 | 65.5 | 202 | 22 | US-09-791-537-45471 | Sequence 45471, A |
| 28 | 93 | 65.5 | 202 | 22 | US-09-791-537-45472 | Sequence 45472, A |
| 29 | 93 | 65.5 | 202 | 22 | US-09-791-537-45483 | Sequence 45483, A |
| 30 | 93 | 65.5 | 202 | 22 | US-09-791-537-45484 | Sequence 45484, A |
| 31 | 93 | 65.5 | 202 | 22 | US-09-791-537-45485 | Sequence 45485, A |
| 32 | 93 | 65.5 | 202 | 22 | US-09-791-537-45486 | Sequence 45486, A |
| 33 | 93 | 65.5 | 202 | 22 | US-09-791-537-45487 | Sequence 45487, A |
| 34 | 93 | 65.5 | 202 | 22 | US-09-791-537-45488 | Sequence 45488, A |
| 35 | 93 | 65.5 | 202 | 22 | US-09-791-537-45489 | Sequence 45489, A |
| 36 | 93 | 65.5 | 202 | 22 | US-09-791-537-45490 | Sequence 45490, A |
| 37 | 93 | 65.5 | 202 | 22 | US-09-791-537-45491 | Sequence 45491, A |
| 38 | 93 | 65.5 | 202 | 22 | US-09-791-537-45492 | Sequence 45492, A |
| 39 | 93 | 65.5 | 202 | 22 | US-09-791-537-45493 | Sequence 45493, A |
| 40 | 93 | 65.5 | 202 | 22 | US-09-791-537-45494 | Sequence 45494, A |
| 41 | 93 | 65.5 | 202 | 22 | US-09-791-537-45495 | Sequence 45495, A |
| 42 | 93 | 65.5 | 202 | 22 | US-09-791-537-45496 | Sequence 45496, A |
| 43 | 93 | 65.5 | 202 | 22 | US-09-791-537-45497 | Sequence 45497, A |
| 44 | 93 | 65.5 | 202 | 22 | US-09-791-537-45498 | Sequence 45498, A |
| 45 | 93 | 65.5 | 202 | 22 | US-09-791-537-45499 | Sequence 45499, A |

ALIGNMENTS

RESULT 1
PCT-US01-03540-25
; Sequence 25, Application PC/TUS0103540
; GENERAL INFORMATION:
; APPLICANT: DUKE UNIVERSITY
; TITLE OF INVENTION: HUMAN IMMUNODEFICIENCY VIRUS VACCINE
; FILE REFERENCE: 1579-547
; CURRENT APPLICATION NUMBER: PCT/US01/03540
; PRIOR FILING DATE: 2001-02-05
; PRIOR APPLICATION NUMBER: 09/497,497
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 25
; LENGTH: 27
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US01-03540-25

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 29, 2004, 14:40:26 ; Search time 143 Seconds
(without alignments)
67.921 Million cell updates/sec

Title: US-10-753-339-25
Perfect score: 142
Sequence: 1 KQIINMWQEVGKAMKAFSPVPMF 27

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1599051 seqs, 359727711.residues
Total number of hits satisfying chosen parameters: 1599051

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:
1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
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19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
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| 2 | 142 | 100.0 | 27 | 9 | US-09-775-805-102 |
| 3 | 142 | 100.0 | 27 | 17 | US-10-753-339-25 |
| 4 | 142 | 100.0 | 27 | 17 | US-10-753-339-102 |
| 5 | 90 | 63.4 | 28 | 10 | US-09-966-931-12 |
| 6 | 90 | 63.4 | 28 | 16 | US-10-459-121-12 |
| 7 | 90 | 63.4 | 39 | 9 | US-09-810-310-2 |
| 8 | 90 | 63.4 | 39 | 9 | US-09-810-310-9 |
| 9 | 90 | 63.4 | 496 | 15 | US-10-371-472-12 |
| 10 | 90 | 63.4 | 496 | 15 | US-10-371-472-16 |
| 11 | 90 | 63.4 | 848 | 16 | US-10-325-468-38 |
| 12 | 90 | 63.4 | 849 | 16 | US-10-325-468-15 |
| 13 | 90 | 63.4 | 849 | 16 | US-10-325-468-29 |

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| 14 | 90 | 63.4 | 849 | 16 | US-10-325-468-32 | Sequence 32, Appl |
| 15 | 90 | 63.4 | 853 | 13 | US-10-003-035-33 | Sequence 33, Appl |
| 16 | 90 | 63.4 | 853 | 14 | US-10-286-332A-33 | Sequence 33, Appl |
| 17 | 90 | 63.4 | 853 | 14 | US-10-280-915-33 | Sequence 33, Appl |
| 18 | 90 | 63.4 | 853 | 16 | US-10-286-332A-33 | Sequence 33, Appl |
| 19 | 90 | 63.4 | 855 | 16 | US-10-325-468-25 | Sequence 25, Appl |
| 20 | 90 | 63.4 | 883 | 16 | US-10-441-926-2 | Sequence 2, Appl |
| 21 | 90 | 63.4 | 883 | 16 | US-10-441-949-2 | Sequence 2, Appl |
| 22 | 90 | 63.4 | 1101 | 13 | US-10-003-035-53 | Sequence 53, Appl |
| 23 | 90 | 63.4 | 1101 | 14 | US-10-286-332A-53 | Sequence 53, Appl |
| 24 | 90 | 63.4 | 1101 | 14 | US-10-280-915-53 | Sequence 53, Appl |
| 25 | 90 | 63.4 | 1186 | 13 | US-10-003-035-55 | Sequence 55, Appl |
| 26 | 90 | 63.4 | 1186 | 14 | US-10-286-332A-55 | Sequence 55, Appl |
| 27 | 90 | 63.4 | 1186 | 14 | US-10-280-915-55 | Sequence 55, Appl |
| 28 | 90 | 63.4 | 1186 | 16 | US-10-286-332A-55 | Sequence 55, Appl |
| 29 | 90 | 63.4 | 1186 | 16 | US-10-286-332A-55 | Sequence 55, Appl |
| 30 | 89 | 62.7 | 726 | 14 | US-10-196-515-3 | Sequence 3, Appl |
| 31 | 88 | 62.0 | 25 | 9 | US-09-775-805-29 | Sequence 29, Appl |
| 32 | 88 | 62.0 | 25 | 17 | US-10-753-339-29 | Sequence 29, Appl |
| 33 | 88 | 62.0 | 483 | 15 | US-10-371-472-31 | Sequence 31, Appl |
| 34 | 88 | 62.0 | 487 | 15 | US-10-371-472-33 | Sequence 33, Appl |
| 35 | 88 | 62.0 | 498 | 15 | US-10-371-472-5 | Sequence 5, Appl |
| 36 | 87 | 61.3 | 236 | 10 | US-09-827-688-2 | Sequence 2, Appl |
| 37 | 86 | 60.6 | 28 | 10 | US-09-966-931-4 | Sequence 4, Appl |
| 38 | 86 | 60.6 | 28 | 10 | US-09-966-931-5 | Sequence 5, Appl |
| 39 | 86 | 60.6 | 28 | 10 | US-09-966-931-10 | Sequence 10, Appl |
| 40 | 86 | 60.6 | 28 | 10 | US-09-966-931-11 | Sequence 11, Appl |
| 41 | 86 | 60.6 | 28 | 10 | US-09-966-931-13 | Sequence 13, Appl |
| 42 | 86 | 60.6 | 28 | 10 | US-09-966-931-15 | Sequence 15, Appl |
| 43 | 86 | 60.6 | 28 | 10 | US-09-966-931-21 | Sequence 21, Appl |
| 44 | 86 | 60.6 | 28 | 14 | US-10-105-545-14 | Sequence 14, Appl |
| 45 | 86 | 60.6 | 28 | 16 | US-10-459-121-4 | Sequence 4, Appl |

ALIGNMENTS

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US-09-775-805-25
; Sequence 25, Application US/09775805
; Publication No. US20010036461A1
; GENERAL INFORMATION:
; APPLICANT: DUKE UNIVERSITY
; TITLE OF INVENTION: HUMAN IMMUNODEFICIENCY VIRUS VACCINE
; FILE REFERENCE: 1579-548
; CURRENT APPLICATION NUMBER: US/09/775,805
; CURRENT FILING DATE: 2001-02-05
; PRIOR FILING DATE: 09/497,497
; PRIOR FILING DATE: 2000-02-04
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 25
; LENGTH: 27
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-775-805-25

Query Match 100.0%; Score 142; DB 9; Length 27;
Best Local Similarity 100.0%; Pred. No. 2,1e-14;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KQIINMWQEVGKAMKAFSPVPMF 27
DB 1 KQIINMWQEVGKAMKAFSPVPMF 27

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US-09-775-805-102
; Sequence 102, Application US/09775805
; Publication No. US20010036461A1
; GENERAL INFORMATION:
; APPLICANT: DUKE UNIVERSITY
; TITLE OF INVENTION: HUMAN IMMUNODEFICIENCY VIRUS VACCINE

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 29, 2004, 14:31:10 ; Search time 38 Seconds
(without alignments)
47.121 Million cell updates/sec

Title: US-10-753-339-25

Perfect score: 142

Sequence: 1 KQIINWQEVGKAYAKAPSPVIMPF 27

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

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- 2: /cgn2_6/prodata/1/iaa/5B COMB.pep:*
- 3: /cgn2_6/prodata/1/iaa/6A COMB.pep:*
- 4: /cgn2_6/prodata/1/iaa/6B COMB.pep:*
- 5: /cgn2_6/prodata/1/iaa/PCBUS COMB.pep:*
- 6: /cgn2_6/prodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
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| 1 | 90 | 63.4 | 24 | 2 | US-08-455-625-24 |
| 2 | 90 | 63.4 | 24 | 2 | US-08-407-252-3 |
| 3 | 90 | 63.4 | 24 | 3 | US-08-455-685-24 |
| 4 | 90 | 63.4 | 24 | 3 | US-08-060-988A-24 |
| 5 | 90 | 63.4 | 24 | 4 | US-09-508-552-18 |
| 6 | 90 | 63.4 | 24 | 5 | PCT-US94-05142-24 |
| 7 | 90 | 63.4 | 28 | 1 | US-08-488-252-1 |
| 8 | 90 | 63.4 | 28 | 2 | US-08-448-603A-12 |
| 9 | 90 | 63.4 | 28 | 3 | US-09-134-075-12 |
| 10 | 90 | 63.4 | 28 | 3 | US-09-492-739-12 |
| 11 | 90 | 63.4 | 28 | 5 | PCT-US92-06688-1 |
| 12 | 90 | 63.4 | 39 | 2 | US-08-455-625-2 |
| 13 | 90 | 63.4 | 39 | 2 | US-08-455-685-2 |
| 14 | 90 | 63.4 | 39 | 3 | US-08-455-685-2 |
| 15 | 90 | 63.4 | 39 | 3 | US-08-455-685-2 |
| 16 | 90 | 63.4 | 39 | 3 | US-08-060-988A-2 |
| 17 | 90 | 63.4 | 39 | 3 | US-08-060-988A-28 |
| 18 | 90 | 63.4 | 39 | 4 | US-09-508-552-2 |
| 19 | 90 | 63.4 | 39 | 4 | US-09-508-552-9 |
| 20 | 90 | 63.4 | 39 | 5 | PCT-US94-05142-2 |
| 21 | 90 | 63.4 | 39 | 5 | PCT-US94-05142-28 |
| 22 | 90 | 63.4 | 181 | 5 | PCT-US93-07805-1 |
| 23 | 90 | 63.4 | 496 | 3 | US-08-889-841B-12 |
| 24 | 90 | 63.4 | 496 | 3 | US-08-889-841B-16 |
| 25 | 90 | 63.4 | 496 | 4 | US-09-419-362-12 |
| 26 | 90 | 63.4 | 496 | 4 | US-09-419-362-16 |
| 27 | 90 | 63.4 | 856 | 3 | US-09-124-900-9 |

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| 28 | 90 | 63.4 | 863 | 3 | US-08-463-210-11 | Sequence 11, Appl |
| 29 | 90 | 63.4 | 863 | 4 | US-08-463-028-11 | Sequence 11, Appl |
| 30 | 90 | 63.4 | 880 | 2 | US-08-788-815-7 | Sequence 7, Appl |
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| 32 | 90 | 63.4 | 880 | 4 | US-09-568-105-7 | Sequence 7, Appl |
| 33 | 89 | 62.7 | 28 | 1 | US-08-488-252-7 | Sequence 7, Appl |
| 34 | 89 | 62.7 | 62 | 1 | US-08-105-483-444 | Sequence 444, App |
| 35 | 89 | 62.7 | 62 | 1 | US-08-709-209-444 | Sequence 444, App |
| 36 | 89 | 62.7 | 62 | 1 | US-08-303-275-155 | Sequence 155, App |
| 37 | 89 | 62.7 | 62 | 1 | US-08-458-101-444 | Sequence 444, App |
| 38 | 89 | 62.7 | 519 | 3 | US-08-472-240A-18 | Sequence 18, Appl |
| 39 | 89 | 62.7 | 726 | 4 | US-09-337-387-3 | Sequence 3, Appl |
| 40 | 89 | 62.7 | 865 | 3 | US-07-956-483-13 | Sequence 13, Appl |
| 41 | 89 | 62.7 | 887 | 3 | US-08-472-240A-4 | Sequence 4, Appl |
| 42 | 88 | 62.0 | 483 | 3 | US-08-889-841B-31 | Sequence 31, Appl |
| 43 | 88 | 62.0 | 483 | 4 | US-09-419-362-31 | Sequence 31, Appl |
| 44 | 88 | 62.0 | 487 | 3 | US-08-889-841B-33 | Sequence 33, Appl |
| 45 | 88 | 62.0 | 487 | 4 | US-09-419-362-33 | Sequence 33, Appl |

ALIGNMENTS

RESULT 1

US-08-455-625-24
; Sequence 24, Application US/08455625
; Patent No. 5932218

GENERAL INFORMATION:

APPLICANT: Berzofsky, Jay A.
APPLICANT: Ahlers, Jeffrey D.
APPLICANT: Pendleton, C. D.
APPLICANT: Nara, Peter
APPLICANT: Shirai, Mutsunori
TITLE OF INVENTION: COMPOSITE SYNTHETIC PEPTIDE CONSTRUCT
TITLE OF INVENTION: ELICITING NEUTRALIZING ANTIBODIES AND CYTOTOXIC T
TITLE OF INVENTION: LYMPHOCYTES AGAINST HIV
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Birch, Stewart, Kolasch & Birch
STREET: P.O. Box 747
CITY: Falls Church
STATE: Virginia
COUNTRY: USA
ZIP: 22040-0747

Description

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/455,625
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/060,988
FILING DATE: 14-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: Svensson, Leonard R.
REGISTRATION NUMBER: 30330
REFERENCE/DOCKET NUMBER: 1173-434P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-205-8000
TELEFAX: 703-205-8050
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..24

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 29, 2004, 14:03:20 ; Search time 159 Seconds
(without alignments)
60.916 Million cell updates/sec

Title: US-10-753-339-25

Perfect score: 142

Sequence: 1 KQIINMDEVGKAMYAKAFSPVPMF 27

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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2: Geneseq1990s:*

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8: Geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
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| 2 | 142 | 100.0 | 27 | 4 | AAU12553 Human HIV |
| 3 | 142 | 100.0 | 27 | 5 | AAU70239 HIV Th-CT |
| 4 | 142 | 100.0 | 27 | 5 | AAU70264 HIV gag T |
| 5 | 142 | 100.0 | 137 | 5 | AAU10481 HIV Th-CT |
| 6 | 90 | 63.4 | 24 | 2 | AAE33837 Cluster P |
| 7 | 90 | 63.4 | 24 | 2 | AAE66431 PCLUS 3-1 |
| 8 | 90 | 63.4 | 24 | 2 | AAE66431 HIV-1 CLU |
| 9 | 90 | 63.4 | 24 | 6 | ABG1784 Anti-HIV |
| 10 | 90 | 63.4 | 25 | 1 | AAU11144 Anti-HIV |
| 11 | 90 | 63.4 | 25 | 1 | AAU80749 Sequence |
| 12 | 90 | 63.4 | 28 | 2 | AAW54909 HIV gp120 |
| 13 | 90 | 63.4 | 32 | 2 | AAW76910 Fusion Im |
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| 17 | 90 | 63.4 | 39 | 2 | AAU05339 HIV-1 CLU |
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| 19 | 90 | 63.4 | 39 | 5 | ABG68641 HIV-1 gp1 |
| 20 | 90 | 63.4 | 39 | 5 | ABG68641 HIV-1 gp1 |
| 21 | 90 | 63.4 | 68 | 2 | ABG68648 HIV-1 gp1 |
| 22 | 90 | 63.4 | 117 | 5 | AAU10478 HIV gp120 |
| 23 | 90 | 63.4 | 178 | 2 | AAU10478 HIV/Mouse |
| 24 | 90 | 63.4 | 179 | 1 | AAU22564 Antibody |
| 25 | 90 | 63.4 | 179 | 1 | AAU93537 HIV porti |
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| 26 | 90 | 63.4 | 180 | 4 | AAG78506 |
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| 28 | 90 | 63.4 | 234 | 1 | AAU81143 |
| 29 | 90 | 63.4 | 234 | 1 | AAU92010 |
| 30 | 90 | 63.4 | 234 | 2 | AAU31943 |
| 31 | 90 | 63.4 | 297 | 1 | AAU71198 |
| 32 | 90 | 63.4 | 319 | 1 | AAU71199 |
| 33 | 90 | 63.4 | 353 | 1 | AAU92015 |
| 34 | 90 | 63.4 | 423 | 1 | AAU93536 |
| 35 | 90 | 63.4 | 423 | 1 | AAU92013 |
| 36 | 90 | 63.4 | 496 | 2 | AAU37058 |
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| 40 | 90 | 63.4 | 500 | 7 | AAE39549 |
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| 42 | 90 | 63.4 | 511 | 6 | ABRS5435 |
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ALIGNMENTS

RESULT 1

AAU12476

ID AAU12476 standard; peptide; 27 AA.

XX AAU12476;

AC AAU12476;

XX AAU12476;

DT 27-SEP-2001 (first entry)

XX HIV Th-CTL peptide prototype vaccine immunogen #13.

XX Human immunodeficiency virus; HIV; immunogen; vaccine; anti-HIV;

KW human leukocyte antigen; HLA; T-helper epitope; CTL; Th; epitope;

KW major histocompatibility complex; MHC; cytotoxic T-lymphocyte;

KW Vaccinia ankara.

XX Homo sapiens.

OS Homo sapiens.

XX WO200156355-A2.

PN WO200156355-A2.

XX 09-AUG-2001.

XX 05-FEB-2001; 2001WO-US003540.

XX 04-FEB-2000; 2000US-00497497.

XX (UYDU-) UNIV DUKE.

XX Haynes BF, Liao H;

XX WPI; 2001-489827/53.

XX Vaccine for immunizing against human immunodeficiency virus has mixture

XX or linear array of peptides comprising immunodominant T-helper epitopes

XX and major histocompatibility complex cytotoxic T-lymphocyte epitopes.

XX Claim 1; Page 24; 33pp; English.

XX The present invention relates to human immunodeficiency virus (HIV) and

XX in particular to a human leukocyte antigen (HLA)-based HIV vaccine. The

XX vaccine comprises a mixture of linear array of peptides, or its variants,

XX where the peptides contain immunodominant T-helper (Th) epitopes and

XX major histocompatibility complex (MHC) cytotoxic T-lymphocyte (CTL)

XX epitopes and the linear array of peptides are preferably expressed in

XX modified Vaccinia ankara. The vaccine is useful for immunising a patient

XX against HIV and focuses immune response on many dominant and subdominant

XX CTL epitopes of HIV. DNA or live vectors with linear arrays of CTL

XX epitopes can be used as either primes or boosts of peptides or of each

XX other to optimally give CTL anti-HIV responses. The vaccine induces